## REMARKS

Reconsideration and withdrawal of the rejections of this application and consideration and entry of this paper are respectfully requested in view of the herein remarks, which place the application in condition for allowance.

### 1. Status Of Claims And Formal Matters

Claims 1-8, 10-14 and 16-33 are under consideration in this application. Claim 1 has been amended. No new matter has been added by this amendment.

Support for the recitation that the truncated Mtu *recA* intein is ΔI-CM or ΔI-SM is found on page 12, line 28, page 13, line 1, page 17, line 29, page 24, lines 5-9, page 26, lines 28-30, page 36, lines 7-9 and 23-26 and Figure 2 of the specification as originally filed. Support for a full-length Mtu *recA* intein having a V67L and/or a D422G mutation(s) is found on page 24, lines 10-30 and page 26, lines 28-30 of the specification as originally filed.

Applicants thank the Examiner for withdrawing the objection of claim 11-33 for being improper multiple dependent claims.

It is submitted that the claims, herewith and as originally presented, are patentably distinct over the prior art cited by the Examiner, and that these claims were in full compliance with the requirements of 35 U.S.C. § 112. The amendments of the claims, as presented herein, are not made for purposes of patentability within the meaning of 35 U.S.C. §§§§ 101, 102, 103 or 112. Rather, these amendments and additions are made simply for clarification and to round out the scope of protection to which Applicants are entitled.

### 2. The Rejections Under 35 U.S.C. § 112, First Paragraph, Are Overcome

Claims 1-8, 10, 11-14 and 16-33 were rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing failing to comply with the written description requirement. This rejection is respectfully traversed. This rejection is moot in light of the amendments to the claims submitted herein.

The Examiner alleges that the claims encompass truncated Mtu inteins with the endonuclease domain deleted, and V67L and/or D422G mutations or any intein having a D to G mutation in a location corresponding to residue 422 of the full-length Mtu intein, or any mutein using the homology limitation which is "very similar" to the muteins recited above. The

Examiner further contends that the specification and claims do not indicate what distinguishing attributes are shared by the members of the genus and thus, the scope of the claims include numerous structural variants, and the genus is highly variant because a significant number of structural differences between genus members is permitted.

Although the Applicants do not agree with the Examiner, in the interest of expediting prosecution, claim 1 has been clarified to recite a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). Therefore, the genus of inteins is the truncated Mtu intein ΔI-CM, the truncated Mtu intein ΔI-SM, a full-length intein having a V67L mutation, a full-length intein having a D422G mutation, and a full-length intein having both V67L and D422G mutations.

Applicants submitted concurrently as Exhibits 1-4 to demonstrate that one of ordinary skill in the art can make the inteins of the present invention by combining the teachings of the specification with what was known to one of ordinary skill in the art at the effective filing date. Specifically, Applicants demonstrate that one of ordinary skill in the art can take the teachings of the specification and apply it to what was known in the art to make the inteins of the present invention.

The amino acid sequence of the Applicants cite Davis et al. (Cell. 1992 Oct 16;71(2):201-10 submitted as reference AQ in the Information Disclosure Statement filed April 19, 2001) as a reference for the active, full-length Mtu *recA* intein (page 35, lines 30-31 of the specification). The Medline abstract of the Davis reference is attached hereto as Exhibit 1. In the upper-right hand corner of the Medline abstract is a hyperlink for "Links". Clicking the "Links" hyperlink reveals a submenu of hyperlinks and "Protein" is one of the hyperlinks. Upon clicking the "Protein" hyperlink, two Entrez Protein database submissions for the RecA protein P26345 and S18206 are revealed, attached hereto as Exhibit 2. The entry for Entrez Protein accession number P26345 is attached hereto as Exhibit 3. On the fifth page, line 22 of Exhibit 3, there is a hyperlink labeled "Region" that corresponds to the mature chain of the Endonuclease PI-MtuI. Upon clicking of the above-mentioned "Region" hyperlink, an entry for the Endonuclease PI-MtuI (Mtu recA intein) is revealed and attached hereto as Exhibit 4. The full-length sequence of

the Mtu *recA* intein is on the sixth page of Exhibit 4. The valine (V) at position 67 and the aspartic acid (D) at position 422 are indicated by double underlining.

The characteristics of ΔI-CM or ΔI-SM are described in the specification as originally filed (see, e.g., page 12, line 28, page 13, line 1, page 17, line 29, page 24, lines 5-9, page 26, lines 28-30, page 36, lines 7-9 and 23-26 and Figure 2). The sequence of the ΔI-CM or ΔI-SM inteins can be constructed with the amino acid sequence of full-length Mtu *recA* intein when combined with the teachings of the specification. The ΔI intein is described as the first 110 and the last 58 amino acids of the Mtu *recA* intein (see, e.g., page 36, lines 2-3 and Derbyshire et al., Proc Natl Acad Sci U S A. 1997 Oct 14;94(21):11466-71 submitted as reference CS in an Information Disclosure statement filed April 19, 2001). The mutations identified in ΔI-CM and ΔI-SM are also described (see, e.g., page 36, lines 9 and 24-26). Therefore, Applicants submit that the description in the specification suffices for one of skill in the art to make and use the truncated Mtu inteins ΔI-CM or ΔI-SM.

Applicants also submit that the description in the specification for full-length Mtu *recA* inteins having a V67L and/or a D422G mutation(s) is sufficient for one of ordinary skill in the art to make the full-length mutein inteins without undue experimentation. Applicants identified novel mutations V67L and D422G that affect intein splicing activity and/or controllable cleavage activity. The amino acid sequence of the full-length Mtu *recA* intein was known to one of ordinary skill in the art (as discussed *supra*). Thus, a full-length Mtu *recA* intein having a V67L and/or a D422G mutation(s)can be constructed by one of ordinary skill in the art without undue experimentation.

It is believed that the rejections under 35 U.S.C. § 112, first paragraph, have been overcome. Reconsideration and withdrawal are requested.

## 5. The Rejections Under 35 U.S.C. § 102(e) Are Overcome

Claims 1-8, 11-14 and 16-33 were rejected under 35 U.S.C. §102(e) as allegedly anticipated by Comb *et al.* (U.S. Patent No. 5,834,247, hereinafter "Comb"). This rejection is respectfully traversed. This rejection is moot in light of the amendments to the claims submitted herein. The cited reference does not anticipate the instant invention.

The Examiner alleges that the molecule disclosed by Comb is a non-naturally occurring intein which is "very similar" to a Mtu intein with the endonuclease domain deleted, and V67L

and/or D422G mutation or any intein having a D to G mutation in a location corresponding to residue 422 of the full-length Mtu intein.

The instant invention relates to a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). The intein of the present invention is not disclosed, suggested or enabled by Comb.

It is respectfully pointed out that a two-prong inquiry must be satisfied in order for a Section 102 rejection to stand. First, the prior art reference must contain all of the elements of the claimed invention. *See Lewmar Marine Inc. v. Barient Inc.,* 3 U.S.P.Q.2d 1766 (Fed. Cir. 1987). Second, the prior art must contain an enabling disclosure. *See Chester v. Miller,* 15 U.S.P.Q.2d 1333, 1336 (Fed. Cir. 1990). A reference contains an enabling disclosure if a person of ordinary skill in the art could have combined the description of the invention in the prior art reference with his own knowledge of the art to have placed himself in possession of the invention. *See In re Donohue*, 226, U.S.P.Q. 619, 621 (Fed. Cir. 1985).

Applying the law to the instant facts, the reference relied upon by the Office Action does not disclose, suggest or enable Applicants' invention. Comb does not teach, suggest or enable a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). These mutations enable rapid cleaving in this intein and gives them superior capabilities to the inteins of Combs.

Comb does not teach, suggest or enable any D (aspartic acid) to G (glycine) or V (valine) to L (leucine) mutations. The only substitution mutations that Comb illustrates are (1) a single amino acid change at the serine 1082 of CIVPS2 (col. 11, line 31-33), (2) amino acid substitutions for the threonine 1472 residue of CIVPS2 (col. 11, lines 49-53), (3) an arginine substitution at position 1079 of CIVPS2 (col. 12, lines 40-43), and (4) an alanine substitution for the aspartate 1236 residue (col. 13, lines 54-57). Thus, Comb does not contain all of the elements of the presently claimed invention.

Consequently, reconsideration and withdrawal of the Section 102 rejections are earnestly requested.

## REQUEST FOR INTERVIEW

If any issue remains as an impediment to allowance, a further interview with the Examiner and SPE are respectfully requested; and, the Examiner is additionally requested to contact the undersigned to arrange a mutually convenient time and manner for such an interview.

## CONCLUSION

In view of the remarks and amendments herewith, the application is believed to be in condition for allowance. Favorable reconsideration of the application and prompt issuance of a Notice of Allowance are earnestly solicited. The undersigned looks forward to hearing favorably from the Examiner at an early date, and, the Examiner is invited to telephonically contact the undersigned to advance prosecution. The Commission is authorized to charge any fee occasioned by this paper, or credit any overpayment of such fees, to Deposit Account No. 50-0320.

Respectfully submitted,
FROMMER LAWRENCE & HAUG LLP

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Deborah L. Lu
Reg. No. 50,940
Telephone: (212) 588-0800
Facsimile: (212) 588-0500

# EXHIBIT 1

Cell. 1992 Oct 16;71(2):201-10. Related Articles, Links

## Protein splicing in the maturation of M. tuberculosis recA protein: a mechanism for tolerating a novel class of intervening sequence.

**Davis EO, Jenner PJ, Brooks PC, Colston MJ, Sedgwick SG.**

Laboratory for Leprosy and Mycobacterial Research, National Institute for Medical Research, Mill Hill, London, England.

The M. tuberculosis recA locus comprises an 85 kd open reading frame but produced 38 kd RecA and 47 kd products in E. coli. No RNA processing was detected; rather, an 85 kd precursor protein was spliced, releasing a 47 kd spacer protein, and joining its terminal fragments to form mature RecA protein. "Spacer" protein was also produced in M. tuberculosis and from a hybrid spacer-LacZ alpha fusion molecule. Mutagenesis at codon wobble positions at one splice junction showed that protein rather than nucleotide sequence determined splicing activity. Other mutants defined additional regions needed for splicing and allowed processing to be followed. Splicing was essential for RecA activity in E. coli. The possibility that splicing is a manifestation of a novel class of genetic element is discussed.

PMID: 1423588 [PubMed - indexed for MEDLINE]

# EXHIBIT 2

☐ **1:** P26345 BLink, Domains, Links
RecA protein (Recombinase A) [Contains: Endonuclease PI-MtuI (Mtu recA intein)]
gi|132229|sp|P26345|RECA_MYCTU[132229]

☐ **2:** S18206 BLink, Domains, Links
recombination protein recA precursor - Mycobacterium tuberculosis (strain H37RV)
gi|98821|pir||S18206[98821]

# EXHIBIT 3

LOCUS P26345 790 aa linear BCT 15-MAR-2004
DEFINITION RecA protein (Recombinase A) [Contains: Endonuclease PI-MtuI (Mtu recA intein)].
ACCESSION P26345
VERSION P26345 GI:132229
DBSOURCE swissprot: locus RECA_MYCTU, accession P26345;
class: standard.
extra accessions:O34519,created: May 1, 1992.
sequence updated: May 1, 1992.
annotation updated: Mar 15, 2004.
xrefs: gi: 44661, gi: 44662, gi: 2597999, gi: 2598000, gi: 2598001, gi: 2598002, gi: 41353422, gi: 2624258, gi: 13882564, gi: 13882569, gi: 31619300, gi: 31619503, gi: 98821, pdb accession 1G18, pdb accession 1G19, pdb accession 1MO3, pdb accession 1MO4, pdb accession 1MO5, pdb accession 1MO6
xrefs (non-sequence databases): REBASE2629, TIGRMT2806, TubercuListRv2737c, HAMAPMF_00268, InterProIPR003593, InterProIPR003587, InterProIPR003586, InterProIPR006142, InterProIPR004042, InterProIPR006141, InterProIPR001553, PfamPF00154, PRINTSPR00379, PRINTSPR00142, ProDomPD000229, SMARTSM00382, SMARTSM00305, SMARTSM00306, TIGRFAMsTIGR01443, TIGRFAMsTIGR01445, PROSITEPS50818, PROSITEPS50819, PROSITEPS50817, PROSITEPS00321, PROSITEPS50162, PROSITEPS50163
KEYWORDS DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding; Autocatalytic cleavage; Protein splicing; Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome; 3D-structure.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (residues 1 to 790)
AUTHORS Davis,E.O., Sedgwick,S.G. and Colston,M.J.
TITLE Novel structure of the recA locus of Mycobacterium tuberculosis implies processing of the gene product
JOURNAL J. Bacteriol. 173 (18), 5653-5662 (1991)

MEDLINE 91358354
PUBMED 1909321
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv
REFERENCE 2 (residues 1 to 790)
AUTHORS Vansoolingen,D., Hoogenboezem,T., Dehaas,P.E. and Hermans,P.W.M.
TITLE Direct Submission
JOURNAL Submitted (~JUL-1997)
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=Canetti, and SO93
REFERENCE 3 (residues 1 to 790)
AUTHORS Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry,C.E. III, Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Squares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
TITLE Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
JOURNAL Nature 393 (6685), 537-544 (1998)
MEDLINE 98295987
PUBMED 9634230
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv
REFERENCE 4 (residues 1 to 790)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D.H., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A., Bishai,W., Jacobs,W.R.Jr., Venter,J.C. and Fraser,C.M.
TITLE Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
JOURNAL J. Bacteriol. 184 (19), 5479-5490 (2002)

MEDLINE 22206494
PUBMED 12218036
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh
REFERENCE 5 (residues 1 to 790)
AUTHORS Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H., Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S., Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L., Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and Hewinson,R.G.
TITLE The complete genome sequence of Mycobacterium bovis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7877-7882 (2003)
MEDLINE 22709107
PUBMED 12788972
REMARK SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97
REFERENCE 6 (residues 1 to 790)
AUTHORS Davis,E.O., Jenner,P.J., Brooks,P.C., Colston,M.J. and Sedgwick,S.G.
TITLE Protein splicing in the maturation of M. tuberculosis recA protein: a mechanism for tolerating a novel class of intervening sequence
JOURNAL Cell 71 (2), 201-210 (1992)
MEDLINE 93046621
PUBMED 1423588
REMARK PROTEIN SPLICING.
SPECIES=M.tuberculosis
REFERENCE 7 (residues 1 to 790)
AUTHORS Kumar,R.A., Vaze,M.B., Chandra,N.R., Vijayan,M. and Muniyappa,K.
TITLE Functional characterization of the precursor and spliced forms of RecA protein of Mycobacterium tuberculosis
JOURNAL Biochemistry 35 (6), 1793-1802 (1996)
MEDLINE 96229901
PUBMED 8639660
REMARK CHARACTERIZATION.
SPECIES=M.tuberculosis
REFERENCE 8 (residues 1 to 790)
AUTHORS Colston,M.J. and Davis,E.O.

JOURNAL (in) Bloom,B.R. (Ed.);
TUBERCULOSIS: PATHOGENESIS, PROTECTION AND CONTROL: 217-226;
American Society for Microbiology, Washington D.C. (1994)
REMARK REVIEW.
SPECIES=M.tuberculosis
REFERENCE 9 (residues 1 to 790)
AUTHORS Datta,S., Prabu,M.M., Vaze,M.B., Ganesh,N., Chandra,N.R.,
Muniyappa,K. and Vijayan,M.
TITLE Crystal structures of Mycobacterium tuberculosis RecA and its
complex with ADP-AlF(4): implications for decreased ATPase activity
and molecular aggregation
JOURNAL Nucleic Acids Res. 28 (24), 4964-4973 (2000)
MEDLINE 20572535
PUBMED 11121488
REMARK X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
SPECIES=M.tuberculosis
COMMENT ----------
This SWISS-PROT entry is copyright. It is produced through a
collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from http://www.expasy.ch/sprot
and http://www.ebi.ac.uk/sprot
----------.
[FUNCTION] Can catalyze the hydrolysis of ATP in the presence of
single-stranded DNA, the ATP-dependent uptake of single-stranded
DNA by duplex DNA, and the ATP-dependent hybridization of
homologous single-stranded DNAs. It interacts with lexA causing its
activation and leading to its autocatalytic cleavage.
[FUNCTION] PI-MtuI is an endonuclease.
[SUBCELLULAR LOCATION] Cytoplasmic (By similarity).
[PTM] This protein undergoes a protein self splicing that involves
a post-translational excision of the intervening region (intein)
followed by peptide ligation.
[SIMILARITY] Belongs to the recA family.
[SIMILARITY] In the intein section; belongs to the homing
endonuclease family.
FEATURES Location/Qualifiers

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/db_xref="taxon:1765"
source 1..790
/organism="Mycobacterium tuberculosis"
/db_xref="taxon:1773"
gene 1..790
/gene="RECA"
/note="synonyms: RV2737C, MT2806, MTV002.02C, MB2756C"
Protein 1..790
/gene="RECA"
/product="RecA protein"
/EC_number="3.1.-.-"
Region 1..251
/gene="RECA"
/region_name="Mature chain"
/note="RecA protein, 1st part."
Site 67..74
/gene="RECA"
/site_type="np-binding"
/note="ATP (By similarity)."
Region 252..691
/gene="RECA"
/region_name="Mature chain"
/note="Endonuclease PI-MtuI."
Region 305
/gene="RECA"
/region_name="Variant"
/note="R -> Q (IN STRAINS CANETTI AND SO93)."
Region 430
/gene="RECA"
/region_name="Variant"
/note="A -> L (IN STRAINS CANETTI AND SO93)."
Region 434..435
/gene="RECA"
/region_name="Variant"
/note="QQ -> RR (IN STRAINS CANETTI AND SO93)."

Region 438..439
/gene="RECA"
/region_name="Variant"
/note="IY -> VH (IN STRAINS CANETTI AND SO93)."
Region 692..790
/gene="RECA"
/region_name="Mature chain"
/note="RecA protein, 2nd part."

ORIGIN

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61 rvieiygpes sgkttvalha vanaqaaggv aafidaehal dpdyakklgv dtdsllvsqp
121 dtgeqaleia dmlirsgald ivvidsvaal vpraelegem gdshvglqar lmsqalrkmt
181 galnnsgtta ifinqlrdki gvmfgspett tggkalkfya svrmdvrrve tlkdgtnavg
241 nrtrvkvvkn kclaegtrif dpvtgtthri edvvdgrkpi hvvaaakdgt lharpvvswf
301 dqgtrdvigl riaggaivwa tpdhkvltey gwraagelrk gdrvaqprrf dgfgdsapip
361 adharllgyl igdgrdgwvg gktpinfinv qraliddvtr iaatlgcaah pqgrislaia
421 hrpgerngva dlcqqagiyg klawektipn wffepdiaad ivgnllfglf esdgwvsreq
481 tgalrvgytt tseqlahqih wlllrfgvgs tvrdydptqk rpsivngrri qskrqvfevr
541 isgmdnvtaf aesvpmwgpr gaaliqaipe atqgrrrgsq atylaaemtd avlnylderg
601 vtaqeaaami gvasgdprgg mkqvlgasrl rrdrvqalad alddkflhdm laeelrysvi
661 revlptrrar tfdleveelh tlvaegvvvh ncsppfkqae fdilygkgis regslidmgv
721 dqglirksga wftyegeqlg qgkenarnfl venadvadei ekkikeklgi gavvtddpsn
781 dgvlpapvdf

//

# EXHIBIT 4

LOCUS P26345 440 aa linear BCT 15-MAR-2004
DEFINITION RecA protein (Recombinase A) [Contains: Endonuclease PI-MtuI (Mtu recA intein)].
ACCESSION P26345 REGION: 252..691
VERSION P26345 GI:132229
DBSOURCE swissprot: locus RECA_MYCTU, accession P26345;
class: standard.
extra accessions:O34519,created: May 1, 1992.
sequence updated: May 1, 1992.
annotation updated: Mar 15, 2004.
xrefs: gi: 44661, gi: 44662, gi: 2597999, gi: 2598000, gi: 2598001, gi: 2598002, gi: 41353422, gi: 2624258, gi: 13882564, gi: 13882569, gi: 31619300, gi: 31619503, gi: 98821, pdb accession 1G18, pdb accession 1G19, pdb accession 1MO3, pdb accession 1MO4, pdb accession 1MO5, pdb accession 1MO6
xrefs (non-sequence databases): REBASE2629, TIGRMT2806, TubercuListRv2737c, HAMAPMF_00268, InterProIPR003593, InterProIPR003587, InterProIPR003586, InterProIPR006142, InterProIPR004042, InterProIPR006141, InterProIPR001553, PfamPF00154, PRINTSPR00379, PRINTSPR00142, ProDomPD000229, SMARTSM00382, SMARTSM00305, SMARTSM00306, TIGRFAMsTIGR01443, TIGRFAMsTIGR01445, PROSITEPS50818, PROSITEPS50819, PROSITEPS50817, PROSITEPS00321, PROSITEPS50162, PROSITEPS50163
KEYWORDS DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding; Autocatalytic cleavage; Protein splicing; Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome; 3D-structure.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (residues 1 to 440)
AUTHORS Davis,E.O., Sedgwick,S.G. and Colston,M.J.
TITLE Novel structure of the recA locus of Mycobacterium tuberculosis implies processing of the gene product
JOURNAL J. Bacteriol. 173 (18), 5653-5662 (1991)

MEDLINE 91358354
PUBMED 1909321
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv
REFERENCE 2 (residues 1 to 440)
AUTHORS Vansoolingen,D., Hoogenboezem,T., Dehaas,P.E. and Hermans,P.W.M.
TITLE Direct Submission
JOURNAL Submitted (~JUL-1997)
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=Canetti, and SO93
REFERENCE 3 (residues 1 to 440)
AUTHORS Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry,C.E. III, Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Squares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
TITLE Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
JOURNAL Nature 393 (6685), 537-544 (1998)
MEDLINE 98295987
PUBMED 9634230
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=H37Rv
REFERENCE 4 (residues 1 to 440)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D.H., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A., Bishai,W., Jacobs,W.R.Jr., Venter,J.C. and Fraser,C.M.
TITLE Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
JOURNAL J. Bacteriol. 184 (19), 5479-5490 (2002)

MEDLINE 22206494
PUBMED 12218036
REMARK SEQUENCE FROM N.A.
SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh
REFERENCE 5 (residues 1 to 440)
AUTHORS Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H., Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S., Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L., Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and Hewinson,R.G.
TITLE The complete genome sequence of Mycobacterium bovis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7877-7882 (2003)
MEDLINE 22709107
PUBMED 12788972
REMARK SEQUENCE FROM N.A.
SPECIES=M.bovis; STRAIN=AF2122/97
REFERENCE 6 (residues 1 to 440)
AUTHORS Davis,E.O., Jenner,P.J., Brooks,P.C., Colston,M.J. and Sedgwick,S.G.
TITLE Protein splicing in the maturation of M. tuberculosis recA protein: a mechanism for tolerating a novel class of intervening sequence
JOURNAL Cell 71 (2), 201-210 (1992)
MEDLINE 93046621
PUBMED 1423588
REMARK PROTEIN SPLICING.
SPECIES=M.tuberculosis
REFERENCE 7 (residues 1 to 440)
AUTHORS Kumar,R.A., Vaze,M.B., Chandra,N.R., Vijayan,M. and Muniyappa,K.
TITLE Functional characterization of the precursor and spliced forms of RecA protein of Mycobacterium tuberculosis
JOURNAL Biochemistry 35 (6), 1793-1802 (1996)
MEDLINE 96229901
PUBMED 8639660
REMARK CHARACTERIZATION.
SPECIES=M.tuberculosis
REFERENCE 8 (residues 1 to 440)
AUTHORS Colston,M.J. and Davis,E.O.

JOURNAL (in) Bloom,B.R. (Ed.);
TUBERCULOSIS: PATHOGENESIS, PROTECTION AND CONTROL: 217-226;
American Society for Microbiology, Washington D.C. (1994)
REMARK REVIEW.
SPECIES=M.tuberculosis
REFERENCE 9 (residues 1 to 440)
AUTHORS Datta,S., Prabu,M.M., Vaze,M.B., Ganesh,N., Chandra,N.R.,
Muniyappa,K. and Vijayan,M.
TITLE Crystal structures of Mycobacterium tuberculosis RecA and its
complex with ADP-AlF(4): implications for decreased ATPase activity
and molecular aggregation
JOURNAL Nucleic Acids Res. 28 (24), 4964-4973 (2000)
MEDLINE 20572535
PUBMED 11121488
REMARK X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
SPECIES=M.tuberculosis
COMMENT ----------
This SWISS-PROT entry is copyright. It is produced through a
collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from http://www.expasy.ch/sprot
and http://www.ebi.ac.uk/sprot
----------.
[FUNCTION] Can catalyze the hydrolysis of ATP in the presence of
single-stranded DNA, the ATP-dependent uptake of single-stranded
DNA by duplex DNA, and the ATP-dependent hybridization of
homologous single-stranded DNAs. It interacts with lexA causing its
activation and leading to its autocatalytic cleavage.
[FUNCTION] PI-MtuI is an endonuclease.
[SUBCELLULAR LOCATION] Cytoplasmic (By similarity).
[PTM] This protein undergoes a protein self splicing that involves
a post-translational excision of the intervening region (intein)
followed by peptide ligation.
[SIMILARITY] Belongs to the recA family.
[SIMILARITY] In the intein section; belongs to the homing
endonuclease family.
FEATURES Location/Qualifiers

source 1..440
/organism="Mycobacterium bovis"
/db_xref="taxon:1765"
source 1..440
/organism="Mycobacterium tuberculosis"
/db_xref="taxon:1773"
gene <1..>440
/gene="RECA"
/note="synonyms: RV2737C, MT2806, MTV002.02C, MB2756C"
Protein <1..>440
/gene="RECA"
/product="RecA protein"
/EC_number="3.1.-.-"
Region 1..440
/gene="RECA"
/region_name="Mature chain"
/note="Endonuclease PI-Mtul."
Region 54
/gene="RECA"
/region_name="Variant"
/note="R -> Q (IN STRAINS CANETTI AND SO93)."
Region 179
/gene="RECA"
/region_name="Variant"
/note="A -> L (IN STRAINS CANETTI AND SO93)."
Region 183..184
/gene="RECA"
/region_name="Variant"
/note="QQ -> RR (IN STRAINS CANETTI AND SO93)."
Region 187..188
/gene="RECA"
/region_name="Variant"
/note="IY -> VH (IN STRAINS CANETTI AND SO93)."

ORIGIN

1 claegtrifd pvtgtthrie dvvdgrkpih vvaaakdgtl harpvvswfd qgtrdviglr

61 iaggaivwat pdhkvlteyg wraagelrkg drvaqprrfd gfgdsapipa dharllgyli

121 gdgrdgwvgg ktpinfinvq raliddvtri aatlgcaahp qgrislaiah rpgerngvad

181 lcqqagiygk lawektipnw ffepdiaadi vgnllfglfe sdgwvsreqt galrvgyttt

241 seqlahqihw lllrfgvgst vrdydptqkr psivngrriq skrqvfevri sgmdnvtafa

301 esvpmwgprg aaliqaipea tqgrrrgsqa tylaaemtda vlnyldergv taqeaaamig

361 vasgdprggm kqvlgasrlr rdrvqalada lddkflhdml aeelrysvir evlptrrart

421 fdleveelht lvaegvvvhn